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SEP 0 3 1999

GROUP 1800

This Raw Listing contains the General
Information Section and up to the first 5 pages.

ENTERED

```
 1                         SEQUENCE LISTING
 2
 3   (1)    General Information
 4
 5          (i) APPLICANT: Blinkovsky, Alexander
 6                          Brown, Kimberly
 7                          Golightly, Elizabeth
 8                          Byun, Tony
 9                          Lene V. Kofod
10
11          (ii) TITLE OF THE INVENTION: Polypeptides Having Aminopeptidase
12                    Activity And Nucleic Acids Encoding Same
13
14          (iii) NUMBER OF SEQUENCES: 9
15
16          (iv) CORRESPONDENCE ADDRESS:
17             (A) ADDRESSEE: Novo Nordisk of North America, Inc.
18             (B) STREET: 405 Lexington Avenue
19             (C) CITY: New York
20             (D) STATE: NY
21             (E) COUNTRY: U.S.A.
22             (F) ZIP: 10174
23
24          (v) COMPUTER READABLE FORM:
25             (A) MEDIUM TYPE: Diskette
26             (B) COMPUTER: IBM Compatible
27             (C) OPERATING SYSTEM: DOS
28             (D) SOFTWARE: FastSEQ for Windows Version 2.0
29
30          (vi) CURRENT APPLICATION DATA:
31             (A) APPLICATION NUMBER: To Be Assigned
32             (B) FILING DATE: 15-MAY-1998
33             (C) CLASSIFICATION:
34
35          (vii) PRIOR APPLICATION DATA:
36             (A) APPLICATION NUMBER:
37             (B) FILING DATE:
38
39          (viii) ATTORNEY/AGENT INFORMATION:
40             (A) NAME: Starnes, Robert L
41             (B) REGISTRATION NUMBER: 41,324
42             (C) REFERENCE/DOCKET NUMBER: 5253.200-US
43
44          (ix) TELECOMMUNICATION INFORMATION:
45             (A) TELEPHONE: 212-867-0123
46             (B) TELEFAX: 212-878-9655
```

INPUT SET: S26235.raw

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47                (C) TELEX:
48
49
50    (2) INFORMATION FOR SEQ ID NO:1:
51
52          (i) SEQUENCE CHARACTERISTICS:
53             (A) LENGTH: 1491 base pairs
54             (B) TYPE: nucleic acid
55             (C) STRANDEDNESS: single
56             (D) TOPOLOGY: linear
57
58          (ix) FEATURE:
59
60          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
61
62    ATGAGGTCGC TTTTGTGGGC TTCGTTGCTT TCGGGCGTGT TGGCTGGGAG GGCGCTTGTT      60
63    TCGCCGGATG AGTTCCCCGA GGATATTCAG TTGGAAGATC TGCTGGAAGG ATCCCAACAG     120
64    CTTGAGGACT TCGCCTATGC CTACCCCGAG CGCAATCGCG TCTTTGGTGG TAAAGCCCAC     180
65    GACGACACGG TTAACTATCT CTACGAGGAG CTGAAGAAGA CTGGCTACTA TGATGTCTAC     240
66    AAGCAGCCTC AGGTGCACCT GTGGAGCAAT GCCGACCAGA CGCTCAAGGT GGGCGATGAG     300
67    GAAATCGAGG CGAAGACCAT GACCTACAGT CCCAGCGTCG AGGTCACCGC CGATGTAGCC     360
68    GTCGTCAAGA ACCTGGGATG CAGCGAGGCG GATTACCCAT CCGATGTCGA GGGCAAGGTC     420
69    GCCCTGATCA AGCGTGGAGA ATGCCCGTTC GGCGACAAGT CGGTTCTCGC TGCCAAAGCC     480
70    AAGGCCGCGG CTTCGATTGT CTATAACAAT GTGGCCGGAT CCATGGCGGG CACCCTTGGC     540
71    GCGGCGCAGA GTGATAAGGG ACCGTATTCG GCCATTGTCG GTATCAGCTT GGAGGATGGC     600
72    CAGAAGCTGA TCAAGCTTGC TGAGGCTGGA TCGGTATCTG TGGATCTGTG GGTGGATAGT     660
73    AAGCAGGAGA ACCGTACGAC GTATAACGTT GTCGCGCAGA CGAAGGGCGG CGATCCGAAC     720
74    AACGTCGTCG CGCTGGGTGG CCACACGGAC TCAGTCGAGG CGGGCCCTGG TATCAACGAC     780
75    GATGGCTCGG GCATTATTAG CAACTTGGTC ATTGCCAAAG CGCTCACGCA GTACTCCGTC     840
76    AAGAATGCCG TGCGCTTCCT CTTCTGGACA GCAGAGGAGT TCGGTCTGCT GGGCAGCAAC     900
77    TACTACGTCT CCCATCTGAA TGCCACCGAG CTGAACAAGA TCCGACTGTA CCTGAACTTC     960
78    GACATGATCG CCTCACCTAA CTACGCCCTC ATGATCTATG ACGGTGATGG ATCGGCGTTC    1020
79    AACCAGAGCG GACCGGCCGG TTCCGCCCAG ATCGAGAAAC TGTTCGAGGA CTACTACGAC    1080
80    TCCATCGACC TGCCTCATAT CCCCACCCAG TTTGACGGAC GTTCCGACTA CGAGGCCTTT    1140
81    ATCCTGAACG GCATTCCGTC CGGTGGACTC TTCACGGGCG CCGAGGGCAT CATGTCCGAA    1200
82    GAGAACGCAA GCCGCTGGGG AGGTCAAGCC GGCGTGGCCT ACGACGCCAA CTACCACGCC    1260
83    GCGGGAGACA ACATGACCAA CCTCAACCAT GAAGCCTTCC TGATCAACTC CAAAGCCACC    1320
84    GCCTTCGCCG TCGCCACCTA CGCCAACGAC CTCTCCTCGA TCCCCAAACG GAATACCACA    1380
85    TCCTCCTTGC ACCGACGAGC CCGCACCATG CGACCATTCG GCAAGAGAGC TCCGAAGACA    1440
86    CACGCTCACG TATCAGGATC CGGATGCTGG CATTCTCAAG TCGAGGCATA G             1491
87
88
89    (2) INFORMATION FOR SEQ ID NO:2:
90
91          (i) SEQUENCE CHARACTERISTICS:
92             (A) LENGTH: 496 amino acids
93             (B) TYPE: amino acid
94             (C) STRANDEDNESS: single
95             (D) TOPOLOGY: linear
96
97          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
98
99    Met Arg Ser Leu Leu Trp Ala Ser Leu Leu Ser Gly Val Leu Ala Gly
```

```
100     1                   5                   10                  15
101     Arg Ala Leu Val Ser Pro Asp Glu Phe Pro Glu Asp Ile Gln Leu Glu
102             20                  25                  30
103     Asp Leu Leu Glu Gly Ser Gln Gln Leu Glu Asp Phe Ala Tyr Ala Tyr
104             35                  40                  45
105     Pro Glu Arg Asn Arg Val Phe Gly Gly Lys Ala His Asp Asp Thr Val
106             50                  55                  60
107     Asn Tyr Leu Tyr Glu Glu Leu Lys Lys Thr Gly Tyr Tyr Asp Val Tyr
108     65                  70                  75                  80
109     Lys Gln Pro Gln Val His Leu Trp Ser Asn Ala Asp Gln Thr Leu Lys
110             85                  90                  95
111     Val Gly Asp Glu Glu Ile Glu Ala Lys Thr Met Thr Tyr Ser Pro Ser
112             100                 105                 110
113     Val Glu Val Thr Ala Asp Val Ala Val Val Lys Asn Leu Gly Cys Ser
114             115                 120                 125
115     Glu Ala Asp Tyr Pro Ser Asp Val Glu Gly Lys Val Ala Leu Ile Lys
116             130                 135                 140
117     Arg Gly Glu Cys Pro Phe Gly Asp Lys Ser Val Leu Ala Ala Lys Ala
118     145                 150                 155                 160
119     Lys Ala Ala Ala Ser Ile Val Tyr Asn Asn Val Ala Gly Ser Met Ala
120             165                 170                 175
121     Gly Thr Leu Gly Ala Ala Gln Ser Asp Lys Gly Pro Tyr Ser Ala Ile
122             180                 185                 190
123     Val Gly Ile Ser Leu Glu Asp Gly Gln Lys Leu Ile Lys Leu Ala Glu
124             195                 200                 205
125     Ala Gly Ser Val Ser Val Asp Leu Trp Val Asp Ser Lys Gln Glu Asn
126             210                 215                 220
127     Arg Thr Thr Tyr Asn Val Val Ala Gln Thr Lys Gly Gly Asp Pro Asn
128     225                 230                 235                 240
129     Asn Val Val Ala Leu Gly Gly His Thr Asp Ser Val Glu Ala Gly Pro
130             245                 250                 255
131     Gly Ile Asn Asp Asp Gly Ser Gly Ile Ile Ser Asn Leu Val Ile Ala
132             260                 265                 270
133     Lys Ala Leu Thr Gln Tyr Ser Val Lys Asn Ala Val Arg Phe Leu Phe
134             275                 280                 285
135     Trp Thr Ala Glu Glu Phe Gly Leu Leu Gly Ser Asn Tyr Tyr Val Ser
136             290                 295                 300
137     His Leu Asn Ala Thr Glu Leu Asn Lys Ile Arg Leu Tyr Leu Asn Phe
138     305                 310                 315                 320
139     Asp Met Ile Ala Ser Pro Asn Tyr Ala Leu Met Ile Tyr Asp Gly Asp
140             325                 330                 335
141     Gly Ser Ala Phe Asn Gln Ser Gly Pro Ala Gly Ser Ala Gln Ile Glu
142             340                 345                 350
143     Lys Leu Phe Glu Asp Tyr Tyr Asp Ser Ile Asp Leu Pro His Ile Pro
144             355                 360                 365
145     Thr Gln Phe Asp Gly Arg Ser Asp Tyr Glu Ala Phe Ile Leu Asn Gly
146             370                 375                 380
147     Ile Pro Ser Gly Gly Leu Phe Thr Gly Ala Glu Gly Ile Met Ser Glu
148     385                 390                 395                 400
149     Glu Asn Ala Ser Arg Trp Gly Gly Gln Ala Gly Val Ala Tyr Asp Ala
150             405                 410                 415
151     Asn Tyr His Ala Ala Gly Asp Asn Met Thr Asn Leu Asn His Glu Ala
152             420                 425                 430
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153    Phe Leu Ile Asn Ser Lys Ala Thr Ala Phe Ala Val Ala Thr Tyr Ala
154            435                 440                 445
155    Asn Asp Leu Ser Ser Ile Pro Lys Arg Asn Thr Thr Ser Ser Leu His
156            450                 455                 460
157    Arg Arg Ala Arg Thr Met Arg Pro Phe Gly Lys Arg Ala Pro Lys Thr
158    465                 470                 475                 480
159    His Ala His Val Ser Gly Ser Gly Cys Trp His Ser Gln Val Glu Ala
160            485                 490                 495
161
162
163    (2) INFORMATION FOR SEQ ID NO:3:
164
165            (i) SEQUENCE CHARACTERISTICS:
166              (A) LENGTH: 20 amino acids
167              (B) TYPE: amino acid
168              (C) STRANDEDNESS: single
169              (D) TOPOLOGY: linear
170
171            (ii) MOLECULE TYPE: None
172
173            (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
174
175    Cys Cys Ile Gly Ala Tyr Gly Ala Arg Thr Thr Tyr Cys Cys Ile Gly
176     1               5                   10                  15
177    Ala Arg Gly Ala
178            20
179
180
181
182    (2) INFORMATION FOR SEQ ID NO:4:
183
184            (i) SEQUENCE CHARACTERISTICS:
185              (A) LENGTH: 36 amino acids
186              (B) TYPE: amino acid
187              (C) STRANDEDNESS: single
188              (D) TOPOLOGY: linear
189
190            (ii) MOLECULE TYPE: None
191
192            (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
193
194    Arg Thr Thr Tyr Thr Thr Ile Ala Cys Ile Ala Cys Ile Gly Cys Ile
195     1               5                   10                  15
196    Ala Cys Arg Thr Cys Ile Gly Cys Ile Gly Thr Ile Ala Cys Tyr Thr
197            20                  25                  30
198    Cys Ile Ala Cys
199            35
200
201
202    (2) INFORMATION FOR SEQ ID NO:5:
203
204            (i) SEQUENCE CHARACTERISTICS:
205              (A) LENGTH: 537 amino acids
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INPUT SET: S26235.raw

```
206              (B)  TYPE: amino acid
207              (C)  STRANDEDNESS: single
208              (D)  TOPOLOGY: linear
209
210         (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:
211
212    Met His Phe Ser Leu Lys Gln Leu Ala Val Ala Ala Phe Tyr Ala Thr
213    1               5                   10                  15
214    Asn Leu Gly Ser Ala Tyr Val Ile Pro Gln Phe Phe Gln Glu Ala Phe
215              20                  25                  30
216    Gln Gln Glu Glu Pro Ile Glu Asn Tyr Leu Pro Gln Leu Asn Asp Asp
217              35                  40                  45
218    Asp Ser Ser Ala Val Ala Ala Asn Ile Pro Lys Pro His Ile Pro Tyr
219              50                  55                  60
220    Phe Met Lys Pro His Val Glu Ser Glu Lys Leu Gln Asp Lys Ile Lys
221    65                  70                  75                  80
222    Val Asp Asp Leu Asn Ala Thr Ala Trp Asp Leu Tyr Arg Leu Ala Asn
223              85                  90                  95
224    Tyr Ser Thr Pro Asp Tyr Gly His Pro Thr Arg Val Ile Gly Ser Lys
225              100                 105                 110
226    Gly His Asn Lys Thr Met Glu Tyr Ile Leu Asn Val Phe Asp Asp Met
227              115                 120                 125
228    Gln Asp Tyr Tyr Asp Val Ser Leu Gln Glu Phe Glu Ala Leu Ser Gly
229              130                 135                 140
230    Lys Ile Ile Ser Phe Asn Leu Ser Asp Ala Glu Thr Gly Lys Ser Phe
231    145                 150                 155                 160
232    Ala Asn Thr Thr Ala Phe Ala Leu Ser Pro Pro Val Asp Gly Phe Val
233              165                 170                 175
234    Gly Lys Leu Val Glu Ile Pro Asn Leu Gly Cys Glu Glu Lys Asp Tyr
235              180                 185                 190
236    Ala Ser Val Val Pro Pro Arg His Asn Glu Lys Gln Ile Ala Leu Ile
237              195                 200                 205
238    Glu Arg Gly Lys Cys Pro Phe Gly Asp Lys Ser Asn Leu Ala Gly Lys
239              210                 215                 220
240    Phe Gly Phe Thr Ala Val Val Ile Tyr Asp Asn Glu Pro Lys Ser Lys
241    225                 230                 235                 240
242    Glu Gly Leu His Gly Thr Leu Gly Glu Pro Thr Lys His Thr Val Ala
243              245                 250                 255
244    Thr Val Gly Val Pro Tyr Lys Val Gly Lys Lys Leu Ile Ala Asn Ile
245              260                 265                 270
246    Ala Leu Asn Ile Asp Tyr Ser Leu Tyr Phe Ala Met Asp Ser Tyr Val
247              275                 280                 285
248    Glu Phe Ile Lys Thr Gln Asn Ile Ile Ala Asp Thr Lys His Gly Asp
249              290                 295                 300
250    Pro Asp Asn Ile Val Ala Leu Gly Ala His Ser Asp Ser Val Glu Glu
251    305                 310                 315                 320
252    Gly Pro Gly Ile Asn Asp Asp Gly Ser Gly Thr Ile Ser Leu Leu Asn
253              325                 330                 335
254    Val Ala Lys Gln Leu Thr His Phe Lys Ile Asn Asn Lys Val Arg Phe
255              340                 345                 350
256    Ala Trp Trp Ala Ala Glu Glu Glu Gly Leu Leu Gly Ser Asn Phe Tyr
257              355                 360                 365
258    Ala Tyr Asn Leu Thr Lys Glu Glu Asn Ser Lys Ile Arg Val Phe Met
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SEQUENCE VERIFICATION REPORT
PATENT APPLICATION   *US/09/080,127*

INPUT SET: S26235.raw

Line	Error	Original Text
31	Wrong application Serial Number	(A) APPLICATION NUMBER: To Be Assigned